

(2)

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/761,117

DATE: 02/08/2001
 TIME: 17:26:46

Input Set : A:\Cpg.pto
 Output Set: N:\CRF3\02082001\I761117.raw

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:
 6 (i) APPLICANT: Dalla-Favera, Riccardo
 7 Chaganti, Raju S.K.
 9 (ii) TITLE OF INVENTION: CLONING AND USES OF THE GENETIC LOCUS
 10 bcl-6
 12 (iii) NUMBER OF SEQUENCES: 9
 14 (iv) CORRESPONDENCE ADDRESS:
 15 (A) ADDRESSEE: Cooper & Dunham LLP
 16 (B) STREET: 1185 Avenue of the Americas
 17 (C) CITY: New York
 18 (D) STATE: New York
 19 (E) COUNTRY: United States of America
 20 (F) ZIP: 10036
 22 (v) COMPUTER READABLE FORM:
 23 (A) MEDIUM TYPE: Floppy disk
 24 (B) COMPUTER: IBM PC compatible
 25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 26 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
 28 (vi) CURRENT APPLICATION DATA:
 C--> 29 (A) APPLICATION NUMBER: US/09/761,117
 C--> 30 (B) FILING DATE: 16-Jan-2001
 31 (C) CLASSIFICATION:
 33 (viii) ATTORNEY/AGENT INFORMATION:
 34 (A) NAME: White, John P.
 35 (B) REGISTRATION NUMBER: 28,678
 36 (C) REFERENCE/DOCKET NUMBER: 0575/43771-A-PCT-US-Y
 38 (ix) TELECOMMUNICATION INFORMATION:
 39 (A) TELEPHONE: (212) 278-0400
 40 (B) TELEFAX: (212) 391-0525
 41 (C) TELEX: 422523 COOP UI
 44 (2) INFORMATION FOR SEQ ID NO: 1:
 46 (i) SEQUENCE CHARACTERISTICS:
 47 (A) LENGTH: 3720 base pairs
 48 (B) TYPE: nucleic acid
 49 (C) STRANDEDNESS: double
 50 (D) TOPOLOGY: linear
 52 (ii) MOLECULE TYPE: cDNA
 54 (ix) FEATURE:
 55 (A) NAME/KEY: CDS
 56 (B) LOCATION: 328..2445
 58 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 60 GGCCCCCTCGA GCCTCGAACCC GGAACCTCCA AATCCGAGAC GCTCTGCTTA TGAGGACCTC 60
 62 GAAATATGCC GGCCAGTGAA AAAATCTTAT GGCTTTGAGG GCTTTGGTT GGCCAGGGGC 120
 64 AGTAAAAATC TCGGAGAGCT GACACCAAGT CCTCCCCCTGC CACGTAGCAG TCGTAAAGTC 180
 66 CGAAGCTAA ATTCCGAGAA TTGAGCTCTG TTGATTCTTA GAACTGGGGT TCTTAGAAGT 240
 68 CGTGATGCAA GAAGTTCTA CGAAAGGCCG GACACCAGGT TTTGAGCAAA ATTTGGACT 300

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70	GTGAAGCAAG GCATTGGTGA AGACAAA ATG GCC TCG CCG GCT GAC AGC TGT			351
71	Met Ala Ser Pro Ala Asp Ser Cys			
72	1	5		
74	ATC CAG TTC ACC CGC CAT GCC AGG GAT GTT CTT CTC AAC CTT AAT CGT			399
75	Ile Gln Phe Thr Arg His Ala Arg Asp Val Leu Leu Asn Leu Asn Arg			
76	10	15	20	
78	CTC CGG AGT CGA GAC ATC TTG ACT GAT GTT GTC ATT GTT GTG AGC CGT			447
79	Leu Arg Ser Arg Asp Ile Leu Thr Asp Val Val Ile Val Val Ser Arg			
80	25	30	35	40
82	GAG CAG TTT AGA GCC CAT AAA ACG GTC CTC ATG GCC TGG AGA GCC CTG			495
83	Glu Gln Phe Arg Ala His Lys Thr Val Leu Met Ala Trp Arg Gly Leu			
84	45	50	55	
86	TTC TAT AGC ATC TTT ACA GAC CAG TTG AAA TGC AAC CTT AGT GTG ATC			543
87	Phe Tyr Ser Ile Phe Thr Asp Gln Leu Lys Cys Asn Leu Ser Val Ile			
88	60	65	70	
90	AAT CTA GAT CCT GAG ATC AAC CCT GAG GGA TTC TGC ATC CTC CTG GAC			591
91	Asn Leu Asp Pro Glu Ile Asn Pro Glu Gly Phe Cys Ile Leu Leu Asp			
92	75	80	85	
94	TTC ATG TAC ACA TCT CGG CTC AAT TTG CGG GAG GGC AAC ATC ATG GCT			639
95	Phe Met Tyr Thr Ser Arg Leu Asn Leu Arg Glu Gly Asn Ile Met Ala			
96	90	95	100	
98	GTG ATG GCC ACG GCT ATG TAC CTG CAG ATG GAG CAT GTT GTG GAC ACT			687
99	Val Met Ala Thr Ala Met Tyr Leu Gln Met Glu His Val Val Asp Thr			
100	105	110	115	120
102	TGC CGG AAG TTT ATT AAG GCC AGT GAA GCA GAG ATG GTT TCT GCC ATC			735
103	Cys Arg Lys Phe Ile Lys Ala Ser Glu Ala Glu Met Val Ser Ala Ile			
104	125	130	135	
106	AAG CCT CCT CGT GAA GAG TTC CTC AAC AGC CGG ATG CTG ATG CCC CAA			783
107	Lys Pro Pro Arg Glu Glu Phe Leu Asn Ser Arg Met Leu Met Pro Gln			
108	140	145	150	
110	GAC ATC ATG GCC TAT CGG GGT CGT GAG GTG GTG GAG AAC AAC CTG CCA			831
111	Asp Ile Met Ala Tyr Arg Gly Arg Glu Val Val Glu Asn Asn Leu Pro			
112	155	160	165	
114	CTG AGG AGC GCC CCT GGG TGT GAG AGC AGA GCC TTT GCC CCC AGC CTG			879
115	Leu Arg Ser Ala Pro Gly Cys Glu Ser Arg Ala Phe Ala Pro Ser Leu			
116	170	175	180	
118	TAC AGT GGC CTG TCC ACA CCG CCA GCC TCT TAT TCC ATG TAC AGC CAC			927
119	Tyr Ser Gly Leu Ser Thr Pro Pro Ala Ser Tyr Ser Met Tyr Ser His			
120	185	190	195	200
122	CTC CCT GTC AGC AGC CTC CTC TTC TCC GAT GAG GAG TTT CGG GAT GTC			975
123	Leu Pro Val Ser Ser Leu Leu Phe Ser Asp Glu Glu Phe Arg Asp Val			
124	205	210	215	
126	CGG ATG CCT GTG GCC AAC CCC TTC CCC AAG GAG CGG GCA CTC CCA TGT			1023
127	Arg Met Pro Val Ala Asn Pro Phe Pro Lys Glu Arg Ala Leu Pro Cys			
128	220	225	230	
130	GAT AGT GCC AGG CCA GTC CCT GGT GAG TAC AGC CGG CCG ACT TTG GAG			1071
131	Asp Ser Ala Arg Pro Val Pro Gly Glu Tyr Ser Arg Pro Thr Leu Glu			
132	235	240	245	
134	GTG TCC CCC AAT GTG TGC CAC AGC AAT ATC TAT TCA CCC AAG GAA ACA			1119

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135	Val	Ser	Pro	Asn	Val	Cys	His	Ser	Asn	Ile	Tyr	Ser	Pro	Lys	Glu	Thr	
136	250				255					260							
138	ATC	CCA	GAA	GAG	GCA	CGA	AGT	GAT	ATG	CAC	TAC	AGT	GTG	GCT	GAG	GGC	1167
139	Ile	Pro	Glu	Glu	Ala	Arg	Ser	Asp	Met	His	Tyr	Ser	Val	Ala	Glu	Gly	
140	265				270					275			280				
142	CTC	AAA	CCT	GCT	GCC	CCC	TCA	GCC	CGA	AAT	GCC	CCC	TAC	TTC	CCT	TGT	1215
143	Leu	Lys	Pro	Ala	Ala	Pro	Ser	Ala	Arg	Asn	Ala	Pro	Tyr	Phe	Pro	Cys	
144					285					290			295				
146	GAC	AAG	GCC	AGC	AAA	GAA	GAA	GAG	AGA	CCC	TCC	TCG	GAA	GAT	GAG	ATT	1263
147	Asp	Lys	Ala	Ser	Lys	Glu	Glu	Glu	Arg	Pro	Ser	Ser	Glu	Asp	Glu	Ile	
148					300					305			310				
150	GCC	CTG	CAT	TTC	GAG	CCC	CCC	AAT	GCA	CCC	CTG	AAC	CGG	AAG	GGT	CTG	1311
151	Ala	Leu	His	Phe	Glu	Pro	Pro	Asn	Ala	Pro	Leu	Asn	Arg	Lys	Gly	Leu	
152					315					320			325				
154	GTT	AGT	CCA	CAG	AGC	CCC	CAG	AAA	TCT	GAC	TGC	CAG	CCC	AAC	TCG	CCC	1359
155	Val	Ser	Pro	Gln	Ser	Pro	Gln	Lys	Ser	Asp	Cys	Gln	Pro	Asn	Ser	Pro	
156					330					335			340				
158	ACA	GAG	GCC	TGC	AGC	AGT	AAG	AAT	GCC	TGC	ATC	CTC	CAG	GGT	TCT	GGC	1407
159	Thr	Glu	Ala	Cys	Ser	Ser	Lys	Asn	Ala	Cys	Ile	Leu	Gln	Gly	Ser	Gly	
160					345					350			355			360	
162	TCC	CCT	CCA	GCC	AAG	AGC	CCC	ACT	GAC	CCC	AAA	GCC	TGC	AGC	TGG	AAG	1455
163	Ser	Pro	Pro	Ala	Lys	Ser	Pro	Thr	Asp	Pro	Lys	Ala	Cys	Ser	Trp	Lys	
164					365					370			375				
166	AAA	TAC	AAG	TTC	ATC	GTG	CTC	AAC	AGC	CTC	AAC	CAG	AAT	GCC	AAA	CCA	1503
167	Lys	Tyr	Lys	Phe	Ile	Val	Leu	Asn	Ser	Leu	Asn	Gln	Asn	Ala	Lys	Pro	
168					380					385			390				
170	GGG	GGG	CCT	GAG	CAG	GCT	GAG	CTG	GGC	CGC	CTT	TCC	CCA	CGA	GCC	TAC	1551
171	Gly	Gly	Pro	Glu	Gln	Ala	Glu	Leu	Gly	Arg	Leu	Ser	Pro	Arg	Ala	Tyr	
172					395					400			405				
174	ACG	GCC	CCA	CCT	GCC	TGC	CAG	CCA	CCC	ATG	GAG	CCT	GAG	AAC	CTT	GAC	1599
175	Thr	Ala	Pro	Pro	Ala	Cys	Gln	Pro	Pro	Met	Glu	Pro	Glu	Asn	Leu	Asp	
176					410					415			420				
178	CTC	CAG	TCC	CCA	ACC	AAG	CTG	AGT	GCC	AGC	GGG	GAG	GAC	TCC	ACC	ATC	
179	Leu	Gln	Ser	Pro	Thr	Lys	Leu	Ser	Ala	Ser	Gly	Glu	Asp	Ser	Thr	Ile	
180					425					430			435			440	
182	CCA	CAA	GCC	AGC	CGG	CTC	AAT	AAC	ATC	GTT	AAC	AGG	TCC	ATG	ACG	GGC	1695
183	Pro	Gln	Ala	Ser	Arg	Leu	Asn	Asn	Ile	Val	Asn	Arg	Ser	Met	Thr	Gly	
184					445					450			455				
186	TCT	CCC	CGC	AGC	AGC	AGC	GAG	AGC	CAC	TCA	CCA	CTC	TAC	ATG	CAC	CCC	1743
187	Ser	Pro	Arg	Ser	Ser	Ser	Glu	Ser	His	Ser	Pro	Leu	Tyr	Met	His	Pro	
188					460					465			470				
190	CCG	AAG	TGC	ACG	TCC	TGC	GGC	TCT	CAG	TCC	CCA	CAG	CAT	GCA	GAG	ATG	1791
191	Pro	Lys	Cys	Thr	Ser	Cys	Gly	Ser	Gln	Ser	Pro	Gln	His	Ala	Glu	Met	
192					475					480			485				
194	TGC	CTC	CAC	ACC	GCT	GGC	CCC	ACG	TTC	GCT	GAG	GAG	ATG	GGA	GAG	ACC	1839
195	Cys	Leu	His	Thr	Ala	Gly	Pro	Thr	Phe	Ala	Glu	Glu	Met	Gly	Glu	Thr	
196					490					495			500				
198	CAG	TCT	GAG	TAC	TCA	GAT	TCT	AGC	TGT	GAG	AAC	GGG	GCC	TTC	TGC		1887
199	Gln	Ser	Glu	Tyr	Ser	Asp	Ser	Ser	Cys	Glu	Asn	Gly	Ala	Phe	Phe	Cys	

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200	505	510	515	520													
202	AAT	GAG	TGT	GAC	TGC	CGC	TTC	TCT	GAG	GAG	GCC	TCA	CTC	AAG	AGG	CAC	1935
203	Asn	Glu	Cys	Asp	Cys	Arg	Phe	Ser	Glu	Glu	Ala	Ser	Leu	Lys	Arg	His	
204																535	
206	ACG	CTG	CAG	ACC	CAC	AGT	GAC	AAA	CCC	TAC	AAG	TGT	GAC	CGC	TGC	CAG	1983
207	Thr	Leu	Gln	Thr	His	Ser	Asp	Lys	Pro	Tyr	Lys	Cys	Asp	Arg	Cys	Gln	
208																550	
210	GCC	TCC	TTC	CGC	TAC	AAG	GGC	AAC	CTC	GCC	AGC	CAC	AAG	ACC	GTC	CAT	2031
211	Ala	Ser	Phe	Arg	Tyr	Lys	Gly	Asn	Leu	Ala	Ser	His	Lys	Thr	Val	His	
212																565	
214	ACC	GGT	GAG	AAA	CCC	TAT	CGT	TGC	AAC	ATC	TGT	GGG	GCC	CAG	TTC	AAC	2079
215	Thr	Gly	Glu	Lys	Pro	Tyr	Arg	Cys	Asn	Ile	Cys	Gly	Ala	Gln	Phe	Asn	
216																575	
218	CGG	CCA	GCC	AAC	CTG	AAA	ACC	CAC	ACT	CGA	ATT	CAC	TCT	GGA	GAG	AAG	2127
219	Arg	Pro	Ala	Asn	Leu	Lys	Thr	His	Thr	Arg	Ile	His	Ser	Gly	Glu	Lys	
220																590	
222	CCC	TAC	AAA	TGC	GAA	ACC	TGC	GGA	GCC	AGA	TTT	GTA	CAG	GTG	GCC	CAC	2175
223	Pro	Tyr	Lys	Cys	Glu	Thr	Cys	Gly	Ala	Arg	Phe	Val	Gln	Val	Ala	His	
224																605	
226	CTC	CGT	GCC	CAT	GTG	CTT	ATC	CAC	ACT	GGT	GAG	AAG	CCC	TAT	CCC	TGT	2223
227	Leu	Arg	Ala	His	Val	Leu	Ile	His	Thr	Gly	Glu	Lys	Pro	Tyr	Pro	Cys	
228																620	
230	GAA	ATC	TGT	GGC	ACC	CGT	TTC	CGG	CAC	CTT	CAG	ACT	CTG	AAG	AGC	CAC	2271
231	Glu	Ile	Cys	Gly	Thr	Arg	Phe	Arg	His	Leu	Gln	Thr	Leu	Lys	Ser	His	
232																635	
234	CTG	CGA	ATC	CAC	ACA	GGA	GAG	AAA	CCT	TAC	CAT	TGT	GAG	AAG	TGT	AAC	2319
235	Leu	Arg	Ile	His	Thr	Gly	Glu	Lys	Pro	Tyr	His	Cys	Glu	Lys	Cys	Asn	
236																650	
238	CTG	CAT	TTC	CGT	CAC	AAA	AGC	CAG	CTG	CGA	CTT	CAC	TTG	CGC	CAG	AAG	2367
239	Leu	His	Phe	Arg	His	Lys	Ser	Gln	Leu	Arg	Leu	His	Leu	Arg	Gln	Lys	
240																665	
242	CAT	GGC	GCC	ATC	ACC	AAC	ACC	AAG	GTG	CAA	TAC	CGC	GTG	TCA	GCC	ACT	2415
243	His	Gly	Ala	Ile	Thr	Asn	Thr	Lys	Val	Gln	Tyr	Arg	Val	Ser	Ala	Thr	
244																685	
246	GAC	CTG	CCT	CCG	GAG	CTC	CCC	AAA	GCC	TGC	TGAAGCATGG	AGTGTGATG					2465
247	Asp	Leu	Pro	Pro	Glu	Leu	Pro	Lys	Ala	Cys							
248																700	
250	CTTCGTCTC	CAGCCCCCTTC	TCAGAATCTA	CCCAAAGGAT	ACTGTAACAC	TTTACAATGT											2525
252	TCATCCCATG	ATGTAGTGCC	TCTTTCATCC	ACTAGTGCAA	ATCATAGCTG	GGGGTTGGGG											2585
254	GTGGTGGGG	TCGGGGCCTG	GGGGACTGGG	AGCCGAGCA	GCTCCCCCTC	CCCCACTGCC											2645
256	ATAAAACATT	AAGAAAATCA	TATTGCTTCT	TCTCCTATGT	GNNNNNNNNN	NNNNNNNNNN											2705
258	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN											2765
260	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN											2825
262	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN											2885
264	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN											2945
266	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN											3005
268	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN											3065
270	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN											3125
272	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN											3185

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274	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	3245										
276	NTTAAGTAT	TGCATCTGTA	TAAGTAAGAA	AATATTTGT	CTAAAATGCC	TCAGTGTATT	3305									
278	TGTATTTTT	TGCAAGTGGG	GGGTTACAAT	TTACCCAGTG	TGTATTAAGA	AAAACCCAAA	3365									
280	GAACCCAAAA	ATCTCCAGAA	GGAAAAATGT	GTAATTTGT	TCTAGTTTC	AGTTTGATA	3425									
282	TACCCGTACA	ACGTGTCCCT	ACGGTGCCTT	TTTCACGGA	AGTTTCAAT	GATGGGCGAG	3485									
284	CGTGCACCAT	CCCTTTTTGA	AGTGTAGGCA	GACACAGGGA	CTTGAAGTGT	TTACTAACTA	3545									
286	AACTCTCTTT	GGGAATGTT	GTCTCATCCC	ANTCTGCGTC	ATGCTTGTT	GATAACTACT	3605									
288	CCGGAGACAG	GGTTTGGCTG	TGTCTAACT	GCATTACCGC	GTTGTAAAAA	ATAGCTGTAC	3665									
290	CAATATAAGA	ATAAAATGTT	GGAAAGTCGC	AAAAAA	AAAAAA	AAAAAA	3720									
293	(2) INFORMATION FOR SEQ ID NO: 2:															
295	(i) SEQUENCE CHARACTERISTICS:															
296	(A) LENGTH: 706 amino acids															
297	(B) TYPE: amino acid															
298	(D) TOPOLOGY: linear															
300	(ii) MOLECULE TYPE: protein															
302	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:															
304	Met	Ala	Ser	Pro	Ala	Asp	Ser	Cys	Ile	Gln	Phe	Thr	Arg	His	Ala	Arg
305	1				5				10				15			
307	Asp	Val	Leu	Leu	Asn	Leu	Asn	Arg	Leu	Arg	Ser	Arg	Asp	Ile	Leu	Thr
308					20				25				30			
310	Asp	Val	Val	Ile	Val	Val	Ser	Arg	Glu	Gln	Phe	Arg	Ala	His	Lys	Thr
311					35				40				45			
313	Val	Leu	Met	Ala	Trp	Arg	Gly	Leu	Phe	Tyr	Ser	Ile	Phe	Thr	Asp	Gln
314					50				55				60			
316	Leu	Lys	Cys	Asn	Leu	Ser	Val	Ile	Asn	Leu	Asp	Pro	Glu	Ile	Asn	Pro
317		65				70				75			80			
319	Glu	Gly	Phe	Cys	Ile	Leu	Leu	Asp	Phe	Met	Tyr	Thr	Ser	Arg	Leu	Asn
320					85				90				95			
322	Leu	Arg	Glu	Gly	Asn	Ile	Met	Ala	Val	Met	Ala	Thr	Ala	Met	Tyr	Leu
323					100				105				110			
325	Gln	Met	Glu	His	Val	Val	Asp	Thr	Cys	Arg	Lys	Phe	Ile	Lys	Ala	Ser
326					115				120				125			
328	Glu	Ala	Glu	Met	Val	Ser	Ala	Ile	Lys	Pro	Pro	Arg	Glu	Glu	Phe	Leu
329					130				135				140			
331	Asn	Ser	Arg	Met	Leu	Met	Pro	Gln	Asp	Ile	Met	Ala	Tyr	Gly	Arg	
332		145				150				155			160			
334	Glu	Val	Val	Glu	Asn	Asn	Leu	Pro	Leu	Arg	Ser	Ala	Pro	Gly	Cys	Glu
335					165				170				175			
338	Ser	Arg	Ala	Phe	Ala	Pro	Ser	Leu	Tyr	Ser	Gly	Leu	Ser	Thr	Pro	Pro
339					180				185				190			
341	Ala	Ser	Tyr	Ser	Met	Tyr	Ser	His	Leu	Pro	Val	Ser	Ser	Leu	Leu	Phe
342					195				200				205			
344	Ser	Asp	Glu	Glu	Phe	Arg	Asp	Val	Arg	Met	Pro	Val	Ala	Asn	Pro	Phe
345					210				215				220			
347	Pro	Lys	Glu	Arg	Ala	Leu	Pro	Cys	Asp	Ser	Ala	Arg	Pro	Val	Pro	Gly
348		225				230				235			240			
350	Glu	Tyr	Ser	Arg	Pro	Thr	Leu	Glu	Val	Ser	Pro	Asn	Val	Cys	His	Ser
351					245				250				255			
353	Asn	Ile	Tyr	Ser	Pro	Lys	Glu	Thr	Ile	Pro	Glu	Glu	Ala	Arg	Ser	Asp

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L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
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